

Searching Microarray Expression Data and Genomic Sequence To Find Consensus *Cis*-Acting Sequence Motifs Which Affect Expression Levels

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Microarray data represents an extensive genome wide set of expression results, which may be hard to interpret biologically. As common *cis*-acting elements may govern the transcription of apparently unrelated genes, we have developed a software program to query putative untranscribed regulatory regions, the transcribed RNA sequence and the translated protein sequence for recurring sequence motifs. However, with a sequence as lengthy as a genome, the list of recurring motifs can be quite extensive. Therefore, microarray expression data is used as a filter (using up and down regulation to cluster motifs) to further refine the list of interesting motifs, so the sequences and their regulatory statistical significance can be output to the researcher.

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